SEQUENCE LISTING

<110> University of Victoria Innovation and Developement Corporation
Hintz, William E.
Eades, Caleb Joshua

<120> Mannosidases and Methods for using the Same

<130> 2847-62447-01

<140> 10/089,211
<141> 2002-03-25

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Asp His Ile Ala Ala Val Asp Thr Ser Lys Thr Asn Ala Met Val Ser
            100   105   110

Leu Phe Glu Thr Thr Ile Arg Thr Leu Ala Gly Met Ile Ser Gly Thr
        115   120   125

Asp Leu Leu Lys Gly Pro Ala Ala Gly Leu Val Asp Asp Ser Arg Val
    130   135   140

Asp Val Leu Leu Glu Gln Ser Gln Asn Leu Ala Glu Val Leu Lys Phe
145   150   155   160

Ala Phe Asp Thr Pro Ser Gly Val Pro Thr Asn Met Ile Asn Ile Thr
            165   170   175

Ser Gly Gly Asn Asp Gly Ala Thr Thr Asn Gly Leu Ala Val Thr Gly
            180   185   190

Thr Leu Val Leu Glu Trp Thr Arg Leu Ser Asp Leu Thr Gly Asn Asp
        195   200   205

Glu Thr Ala Arg Leu Ser Gln Arg Ala Glu Asp Thr Leu Leu His Pro
    210   215   220

Glu Pro Ala Gln Thr Glu Pro Phe Pro Gly Leu Ile Gly Ser Ala Val
225   230   235   240

Asn Ile Ala Asp Gly Lys Leu Ala Asn Gly His Ile Ser Trp Asn Gly
            245   250   255

Gly Ala Asp Ser Thr Thr Glu Thr Leu Ile Lys Met Thr Val Thr Asp
            260   265   270

11

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Pro Glu Arg Phe Gly Leu Thr Arg Asp Arg Trp Val Ala Ala Ala Glu
        275                 280             285

Ser Ser Ile Asn His Leu Ala Ser His Pro Ser Thr Arg Pro Asp Val
        290                 295             300

Thr Phe Leu Ala Thr Thr Asn Glu Glu His Gln Leu Gly Leu Thr Ser
305                 310                 315                 320

Gln His Leu Thr Cys Phe Asp Gly Gly Ser Phe Leu Leu Gly Gly Thr
            325                 330                 335

Leu Leu Asp Arg Gln Asp Phe Val Asp Phe Gly Leu Asp Leu Val Ala
            340                 345                 350

Gly Cys His Glu Thr Thr Asn Ser Thr Leu Thr Gly Ile Gly Pro Glu
        355                 360                 365

Gln Phe Ser Trp Asp Pro Asn Gly Val Pro Asp Ser Gln Lys Glu Leu
    370                 375                 380

Phe Glu Arg Ala Gly Phe Thr Ile Asn Ser Gly Gln Thr Ile Leu Arg
385                 390                 395                 400

Pro Glu Val Ile Glu Ser Phe Thr Thr Ala Trp Arg Val Thr Gly Asp
            405                 410                 415

Gly Thr Thr Leu Glu Trp Val Trp Asn Ala Phe Thr Asn Ile Asn Lys
            420                 425                 430

Thr Cys Arg Thr Ala Thr Gly Phe Ala Gly Leu Glu Asn Val Asn Ala
        435                 440                 445

Ala Asn Gly Gly Gly Arg Ile Asp Asn Gln Glu Ser Phe Met Phe Ala
    450                 455                 460

Glu Val Leu Lys Thr Ser Phe Leu Thr Phe Ala Pro Glu Asp Asp Trp
465                 470                 475                 480

Gln Val Gln Lys Gly Ser Gly Asn Thr Phe Val Thr Asn Thr Glu Ala
            485                 490                 495

His Pro Phe Lys Val Thr Thr Pro Gln
            500                 505
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<210>  7
<211>  6
<212>  DNA
<213>  Aspergillus nidulans

<400>  7
gtaagt                                                              6


<210>  8
<211>  6
<212>  DNA
<213>  Aspergillus nidulans

<220>
<221>  variation
<222>  (4)..(4)
<223>  N = A, C, G, or T

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gtangt                                                              6


<210>  9
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<213>  Aspergillus nidulans

<400>  9
gctgac                                                              6


<210>  10
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<400>  10
rctrac                                                              6


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<212>  DNA
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<400>  11
gtacgt                                                              6


<210>  12
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<212>  DNA
<213>  Aspergillus nidulans

<400>  12
actgac                                                              6
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<210> 13
<211> 10
<212> PRT
<213> Asperfillus nidulans

<400> 13
Gly Gly Leu Gly Glu Ser Phe Thr Glu Thr
1   5   10

<210> 14
<211> 9
<212> PRT
<213> Aspergillus nidulans

<400> 14
Leu Ala Glu Thr Leu Lys Thr Leu Thr
1   5

<210> 15
<211> 29
<212> DNA
<213> PCR Primer

<220>
<221> y represents c, t, or u; r represents g or a; n represents a, c, g, t, or
u; and h represents a, c, t, or u
<222> (1)..(29)
<223>

<400> 15
ggyggyctng gygartcntt ctacgagta   29

<210> 16
<211> 33
<212> DNA
<213> PCR Primer

<220>
<221> y represents c, t, or u; r represents g or a; n represents a, c, g, t, or
u; and h represents a, c, t, or u
<222> (1)..(33)
<223>

<400> 16
gtanaggtac ttnagngtct cngcnagrha gaa   33

<210> 17
<211> 2032
<212> DNA
<213> Aspergillus nidulans

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atcgatgtct gctgcataaa ggcagacgga ggaagatgcc gagacggtgg tcctccctca   60

tcagcatcac agccatcttc ttggtcctct tcttcctcct tcataggaat acagacacac   120

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cacgcgccgc caatagggct acaaacggcc ctgccaacgg ctttgctagg cagcaaagca      180

tatgtccatc aacacccct cagcctccat ataaccgaac cagcacggga gggttcaact       240

ggggtgaaat cccagtcaga taccctgtat ccgacttcat cccgctgtca accaactctc      300

ctgcaacact tccgcgcatc caacgctctt ccttcccact tcaatcctca atcactaaat      360

cccgccaggc agcagtcaaa ggtgcctttc agcgcgcatg gacctcctac acaacccacg      420

cctggaaggc ggacgaggta cggcccatca cggccggatc tcgaaacaac tttggcggat      480

ggggagcgac cctagtcgac aatctcgaca cactgctaat catggggctg gacgaggagt      540

tcgcagcggc agtcgacgcg ctcgcagata tagaattcag cccgcactcg tccccatcct      600

cctcccagag cacaatcaac atattcgaaa cgacaatccg gtatctgggc ggcttgctcg      660

cggcgtatga tctcactggc tgtcgagaga ctcggctgct ggacaaagca atccagcttg      720

gggagatgat ctacacctcc ttcgacacag agaaccgcat gcccgtacca cggtggaatc      780

tgcacaaagc aggcaacgga gagcctcagc gcgcggcagt gcagggcgtg ctcgctgaac      840

tcgccagcag cagtctcgag ttcacgcggc tgtcgcagct gacgggggat atgcggtatt      900

tcgatgcggc atcccgcatt accgatctgc ttgactccca agccggccat acccggatcc      960

cggggttgtg gccagtcagc gtgaacctgc agaaaggcga tctgacccgt gggtcgacat      1020

tcagttttgg cgggatggcc gatagcgcct acgagtatct cggcaagacg tatcggctcc      1080

tcggtggtgt ggggaaaggg ccacagtacg agcgtctggc gcgaaacgca ctagatgccg      1140

ggattcgaca tctcctcttc cgaccgatga cgcctgatca tgcagatatc ctcctacccg      1200

gggtcgcgca cgcaaccagc tcttccgtgg gactcgagcc ccggacagag catctcgcct      1260

gttttgtggg tgggatgtac gcgctcgccg ggaagctttt ctcaaaccag acgtacctcg      1320

acaccggccg gaagctgaca gacggttgta tctggtacta cgataattca ccgctaggta      1380

tcatgccgga gatgttcacc gtgccggctt gtccgtcagt ggctgaatgt ccttgggacg      1440

aaacaagggg tggtatctac acctacgtgc gtgatgggca ctactttctg cgtcctgagg      1500

caatggagag tatcttctat atgtggcgca ttacagggga cgaaaagtac cgcgaggctg      1560

catggagaat gttcacggct atcgaagcgg ttacaaagac ggagtttggg aatgcggcgg      1620

tgcgggatgt tatggttgag gaaggaaatg taaagagaga agatagcatg gagagtttct      1680

ggatggcaga gacgttgaag tatctgtatc tgatatttgg ggagaccgat ttggtcagct      1740

tggacgactg ggtgttcaat acggaggcgc acccctttgag gggtgcaggg agttgacatt      1800

gtattcacac atcggtatag acaaattata gagtagacgt tcaaaacggc caaaactgaa      1860

tggatagact ccatatgcat tgaatataca atgtattcgc tgcaaagcat ggataaaata     1920
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15

aagatgtaca aagtgtcttt gttgtcgctt tgaaagtggt atatcatccc atcataaggt   1980

ggcagtgtaa ccaaccctct atatcaccta catagacagc tgatagaccg gc   2032

<210> 18
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<212> PRT
<213> Aspergillus nidulans

<400> 18
Met Pro Arg Arg Trp Ser Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu

1   5   10   15

Val Leu Phe Phe Leu Leu His Arg Asn Thr Asp Thr Pro Arg Ala Ala
            20   25   30

Asn Arg Ala Thr Asn Gly Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser
            35   40   45

Ile Cys Pro Ser Thr Pro Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr
      50   55   60

Gly Gly Phe Asn Trp Gly Glu Ile Pro Val Arg Tyr Pro Val Ser Asp
65   70   75   80

Phe Ile Pro Leu Ser Thr Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln
                85   90   95

Arg Ser Ser Phe Pro Leu Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala
            100   105   110

Ala Val Lys Gly Ala Phe Gln Arg Ala Trp Tyr Ser Thr Thr Thr His
            115   120   125

Ala Trp Lys Ala Asp Glu Val Arg Pro Ile Thr Ala Gly Ser Arg Asn
      130   135   140

Asn Phe Gly Gly Trp Gly Ala Thr Leu Val Asp Asn Leu Asp Thr Leu
145   150   155   160

Leu Ile Met Gly Leu Asp Glu Glu Phe Ala Ala Ala Val Asp Ala Leu
                165   170   175

Ala Asp Ile Glu Phe Ser Pro His Ser Ser Pro Ser Ser Ser Gln Ser
            180   185   190

16

```
Thr Ile Asn Ile Phe Glu Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu
        195             200             205


Ala Ala Tyr Asp Leu Thr Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys
    210             215             220


Ala Ile Gln Leu Gly Glu Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn
225             230             235                     240


Arg Met Pro Val Pro Arg Trp Asn Leu His Lys Ala Gly Asn Gly Glu
            245             250             255


Pro Gln Arg Ala Ala Val Gln Gly Val Leu Ala Glu Leu Ala Ser Ser
            260             265             270


Ser Leu Glu Phe Thr Arg Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr
        275             280             285


Phe Asp Ala Ala Ser Arg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly
    290             295             300


His Thr Arg Ile Pro Gly Leu Trp Pro Val Ser Val Asn Leu Gln Lys
305             310             315             320


Gly Asp Leu Thr Arg Gly Ser Thr Phe Ser Phe Gly Gly Met Ala Asp
            325             330             335


Ser Ala Tyr Glu Tyr Leu Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val
        340             345             350


Gly Lys Gly Pro Gln Tyr Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala
        355             360             365


Gly Ile Arg His Leu Leu Phe Arg Pro Met Thr Pro Asp His Ala Asp
    370             375             380


Ile Leu Leu Pro Gly Val Ala His Ala Thr Ser Ser Ser Val Gly Leu
385             390             395             400


Glu Pro Arg Thr Glu His Leu Ala Cys Phe Val Gly Gly Met Tyr Ala
            405             410             415


Leu Ala Gly Lys Leu Phe Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg
            420             425             430
```

Lys Leu Thr Asp Gly Cys Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly
        435   440   445

Ile Met Pro Glu Met Phe Thr Val Pro Ala Cys Pro Ser Val Ala Glu
        450   455   460

Cys Pro Trp Asp Glu Thr Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp
465   470   475   480

Gly His Tyr Phe Leu Arg Pro Glu Ala Met Glu Ser Ile Phe Tyr Met
            485   490   495

Trp Arg Ile Thr Gly Asp Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met
        500   505   510

Phe Thr Ala Ile Glu Ala Val Thr Lys Thr Glu Phe Gly Asn Ala Ala
        515   520   525

Val Arg Asp Val Met Val Glu Glu Gly Asn Val Lys Arg Glu Asp Ser
    530   535   540

Met Glu Ser Phe Trp Met Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile
545   550   555   560

Phe Gly Glu Thr Asp Leu Val Ser Leu Asp Asp Trp Val Phe Asn Thr
            565   570   575

Glu Ala His Pro Leu Arg Gly Ala Gly Ser
            580   585

<210> 19
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<213> Artificial Sequence

<220>
<223> Consensus Splice Site

<220>
<221> variation
<222> (1)..(1)
<223> R = G or A

<220>
<221> variation
<222> (4)..(4)
<223> R = G or A

<400> 19
rctrac   6